

# SCORE Search Results Details for Application 10759514 and Search Result us-10-759-514-3.rng.

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This page gives you Search Results detail for the Application 10759514 and Search Result us-10-759-514-3.rng.

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 06:03:13 ; Search time 126.92 Seconds  
(without alignments)  
1260.261 Million cell updates/sec

Title: US-10-759-514-3

Perfect score: 24

Sequence: 1 ccgggagagccatagtggtctgcg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:  
14: geneseqn2005s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	24	100.0	24	10	ADD55637	Add55637 Oligonucl
2	24	100.0	24	10	ADD55641	Add55641 Oligonucl
3	24	100.0	24	14	ADV04767	Adv04767 Synthetic
4	24	100.0	24	14	ADV04754	Adv04754 Synthetic
5	24	100.0	24	14	ADZ75974	Adz75974 Hepatitis
6	24	100.0	24	14	ADZ75978	Adz75978 Hepatitis
c 7	24	100.0	27	2	AAQ64955	Aaq64955 Antisense
c 8	24	100.0	30	2	AAQ64950	Aaq64950 Antisense
9	24	100.0	37	2	AAX37631	Aax37631 HCV detec
10	24	100.0	50	3	AAA52575	Aaa52575 HCV RNA p
c 11	24	100.0	53	2	AAQ98103	Aaq98103 Label ext
c 12	24	100.0	70	2	AAT11268	Aat11268 Hepatitis
c 13	24	100.0	75	14	AEB94147	Aeb94147 Nucleic a
14	24	100.0	86	12	ADJ53747	Adj53747 HBV speci
15	24	100.0	102	4	AAC92379	Aac92379 HCV-RNA W
16	24	100.0	120	2	AAT69054	Aat69054 Hepatitis
c 17	24	100.0	120	14	AEB94144	Aeb94144 Nucleic a
18	24	100.0	120	14	AEB94143	Aeb94143 Nucleic a
19	24	100.0	131	14	ADW15169	Adw15169 HCV H77C
20	24	100.0	131	14	ADW15171	Adw15171 HCV from
21	24	100.0	131	14	ADW15170	Adw15170 HCV from
22	24	100.0	131	14	ADW15174	Adw15174 HCV from
23	24	100.0	131	14	ADW15172	Adw15172 HCV from
24	24	100.0	131	14	ADW15173	Adw15173 HCV from
c 25	24	100.0	140	2	AAT11269	Aat11269 Hepatitis
c 26	24	100.0	155	3	AAZ57775	Aaz57775 Hepatitis
27	24	100.0	159	2	AAQ43062	Aaq43062 -255 to -
28	24	100.0	159	2	AAQ43069	Aaq43069 -255 to -
29	24	100.0	159	2	AAQ43066	Aaq43066 -255 to -
30	24	100.0	159	2	AAQ43071	Aaq43071 -255 to -
31	24	100.0	177	2	AAQ79456	Aaq79456 HCV isola
32	24	100.0	177	2	AAQ68067	Aaq68067 HCV isola
33	24	100.0	177	2	AAQ79452	Aaq79452 HCV isola
34	24	100.0	177	2	AAQ79459	Aaq79459 HCV isola
35	24	100.0	177	2	AAQ79450	Aaq79450 HCV isola
36	24	100.0	177	2	AAQ79451	Aaq79451 HCV isola
37	24	100.0	177	2	AAQ68068	Aaq68068 HCV isola
38	24	100.0	177	2	AAQ79454	Aaq79454 HCV isola
39	24	100.0	177	2	AAQ68069	Aaq68069 HCV isola
40	24	100.0	177	2	AAQ68070	Aaq68070 HCV isola
41	24	100.0	177	2	AAQ79457	Aaq79457 HCV isola
42	24	100.0	177	2	AAQ68063	Aaq68063 HCV isola
43	24	100.0	177	2	AAQ79460	Aaq79460 HCV isola
44	24	100.0	177	2	AAQ79449	Aaq79449 HCV isola
45	24	100.0	177	2	AAQ79455	Aaq79455 HCV isola

#### ALIGNMENTS

RESULT 1

ADD55637

ID ADD55637 standard; DNA; 24 BP.

XX

AC ADD55637;

XX

DT 15-JAN-2004 (first entry)

XX

DE Oligonucleotide probe, PR2 #1, used to detect a HCV nucleic acid.

XX

KW HCV; fluorescent dye; fluorescent molecular beacon pair; lambda phage;

KW lambda phage-HCV hybrid amplicon; detection; diagnosis; HCV infection;  
KW hepatitis; cirrhosis; antiviral therapy; probe; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN US2003104582-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 04-DEC-2001; 2001US-00011855.  
XX  
PR 04-DEC-2001; 2001US-00011855.  
XX  
PA (BAUM//) BAUMANN R.  
PA (HAMD//) HAMDAN H.  
PA (LEWI//) LEWINSKI M.  
XX  
PI Baumann R, Hamdan H, Lewinski M;  
XX  
DR WPI; 2003-801237/75.  
XX  
PT Detecting hepatitis C virus (HCV) nucleic acid in a sample comprises  
PT reverse transcribing and amplifying HCV nucleic acids with primer pair,  
PT hybridizing amplicons with a labeled probe, and detecting a signal.  
XX  
PS Claim 1; Page 10; 11pp; English.  
XX  
CC The invention discloses a method for detecting the presence or amount of  
CC Hepatitis C virus (HCV) nucleic acids in a sample comprising reverse  
CC transcribing and amplifying any HCV nucleic acid present, reacting the  
CC amplified nucleic acids with a probe in the presence of an enzyme that  
CC cleaves the probe if specifically hybridised to HCV nucleic acids, and  
CC detecting a signal from the probe. The detectable label is a fluorescent  
CC dye or a fluorescent molecular beacon pair. Lambda phage HCV nucleic acid  
CC hybrids are introduced into the test sample, reverse transcribed and  
CC amplified using the pair of oligonucleotide primers to produce lambda  
CC phage-HCV hybrid amplicons. The hybrids are hybridised to a control  
CC oligonucleotide sequence (ADD55640) which is conjugated to 6-  
CC carboxyfluorescein (FAM) and 6-carboxytetramethylrhodamine (TAMRA). The  
CC test sample is chosen from serum, blood, plasma, cerebral spinal fluid,  
CC synovial fluid, and urine. The nucleic acids are purified from the sample  
CC prior to the reverse transcription and amplification step. The lambda  
CC phage-HCV ribonucleic acid hybrids may be introduced into the test sample  
CC prior to isolating nucleic acids from the sample. The method is useful  
CC for detecting the presence or amount of hepatitis C virus (HCV) nucleic  
CC acids in a test sample, for diagnosing HCV infection, which can lead to  
CC chronic hepatitis and cirrhosis, for identification of individuals with  
CC high viral replication, for monitoring patients on therapy and for  
CC predicting whether antiviral therapy will be successful. The method is  
CC specific and sensitive and exhibits a broad dynamic range of detection of  
CC HCV nucleic acids and provides quantitative as well as qualitative  
CC results. The sequence presented is an oligonucleotide probe used to  
CC detect HCV nucleic acid.  
XX  
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| ||| |||  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 2  
ADD55641  
ID ADD55641 standard; DNA; 24 BP.  
XX  
AC ADD55641;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Oligonucleotide probe, PR2 #2, used to detect a HCV nucleic acid.  
XX  
KW HCV; fluorescent dye; fluorescent molecular beacon pair; lambda phage;  
KW lambda phage-HCV hybrid amplicon; detection; diagnosis; HCV infection;  
KW hepatitis; cirrhosis; antiviral therapy; probe; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= conjugated to 2'-chloro-7'-phenyl-1,4-  
FT dichloro-6-carboxyfluorescein (VIC)"  
FT modified\_base 24  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= conjugated to 6-  
FT carboxytetramethylrhodamine (TAMRA)"  
XX  
PN US2003104582-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 04-DEC-2001; 2001US-00011855.  
XX  
PR 04-DEC-2001; 2001US-00011855.  
XX  
PA (BAUM/) BAUMANN R.  
PA (HAMD/) HAMDAN H.  
PA (LEWI/) LEWINSKI M.  
XX  
PI Baumann R, Hamdan H, Lewinski M;  
XX  
DR WPI; 2003-801237/75.  
XX  
PT Detecting hepatitis C virus (HCV) nucleic acid in a sample comprises  
PT reverse transcribing and amplifying HCV nucleic acids with primer pair,  
PT hybridizing amplicons with a labeled probe, and detecting a signal.  
XX  
PS Claim 5; Page 10; 11pp; English.  
XX  
CC The invention discloses a method for detecting the presence or amount of  
CC Hepatitis C virus (HCV) nucleic acids in a sample comprising reverse  
CC transcribing and amplifying any HCV nucleic acid present, reacting the  
CC amplified nucleic acids with a probe in the presence of an enzyme that  
CC cleaves the probe if specifically hybridised to HCV nucleic acids, and  
CC detecting a signal from the probe. The detectable label is a fluorescent  
CC dye or a fluorescent molecular beacon pair. Lambda phage HCV nucleic acid  
CC hybrids are introduced into the test sample, reverse transcribed and  
CC amplified using the pair of oligonucleotide primers to produce lambda  
CC phage-HCV hybrid amplicons. The hybrids are hybridised to a control  
CC oligonucleotide sequence (ADD55640) which is conjugated to 6-  
CC carboxyfluorescein (FAM) and 6-carboxytetramethylrhodamine (TAMRA). The

CC test sample is chosen from serum, blood, plasma, cerebral spinal fluid,  
CC synovial fluid, and urine. The nucleic acids are purified from the sample  
CC prior to the reverse transcription and amplification step. The lambda  
CC phage-HCV ribonucleic acid hybrids may be introduced into the test sample  
CC prior to isolating nucleic acids from the sample. The method is useful  
CC for detecting the presence or amount of hepatitis C virus (HCV) nucleic  
CC acids in a test sample, for diagnosing HCV infection, which can lead to  
CC chronic hepatitis and cirrhosis, for identification of individuals with  
CC high viral replication, for monitoring patients on therapy and for  
CC predicting whether antiviral therapy will be successful. The method is  
CC specific and sensitive and exhibits a broad dynamic range of detection of  
CC HCV nucleic acids and provides quantitative as well as qualitative  
CC results. The sequence presented is a labelled oligonucleotide probe used  
CC to detect HCV nucleic acid.

XX

SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| |||  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 3

ADV04767

ID ADV04767 standard; DNA; 24 BP.

XX

AC ADV04767;

XX

DT 24-FEB-2005 (first entry)

XX

DE Synthetic PCR primer #18.

XX

KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.

XX

OS Synthetic.

XX

PN WO2004104198-A1.

XX

PD 02-DEC-2004.

XX

PF 25-NOV-2003; 2003WO-JP015038.

XX

PR 26-MAY-2003; 2003JP-00148242.

PR 19-SEP-2003; 2003JP-00329115.

XX

PA (TORA ) TORAY IND INC.

PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.

PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.

XX

PI Wakita T, Kato T, Date T;

XX

DR WPI; 2005-013292/01.

XX

PT Novel replicon RNA, having sequence of 5' and 3' untranslated region and  
PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic  
PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C  
PT virus infection.

XX

PS Example 7; SEQ ID NO 33; 197pp; Japanese.

XX

CC The invention relates to replicon RNA from genotype 2a of hepatitis C  
CC virus comprising a 5' untranslated region, a base sequence encoding NS3  
CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a  
CC 3' untranslated region. The invention also relates to a cell capable of  
CC reproducing the replicon involving transducing the replicon RNA to a  
CC cell, a method of producing a hepatitis C virus protein, a method of  
CC screening a substance that promotes or suppresses the reproduction of  
CC hepatitis C virus, involving culturing the replicon reproducing cell in  
CC the presence of a test substance, and detecting the reproduction of  
CC replicon RNA in the culture. Virucide. The replicon RNA is useful for  
CC producing a replicon reproduction cell and for increasing the  
CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype  
CC 2a. The cell and the replicon RNA are useful for producing a therapeutic  
CC agent or a diagnostic agent for hepatitis C virus infection, for  
CC producing a vaccine against hepatitis C virus infection and for screening  
CC a substance that promotes or suppresses the reproduction of hepatitis C  
CC virus. This sequence represents a PCR primer used in the scope of the  
CC invention.

XX

SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| ||| |||  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 4

ADV04754

ID ADV04754 standard; DNA; 24 BP.

XX

AC ADV04754;

XX

DT 24-FEB-2005 (first entry)

XX

DE Synthetic PCR primer #5.

XX

KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.

XX

OS Synthetic.

XX

PN WO2004104198-A1.

XX

PD 02-DEC-2004.

XX

PF 25-NOV-2003; 2003WO-JP015038.

XX

PR 26-MAY-2003; 2003JP-00148242.

PR 19-SEP-2003; 2003JP-00329115.

XX

PA (TORA ) TORAY IND INC.

PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.

PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.

XX

PI Wakita T, Kato T, Date T;

XX

DR WPI; 2005-013292/01.

XX

PT Novel replicon RNA, having sequence of 5' and 3' untranslated region and  
PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic  
PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C

PT virus infection.  
XX  
PS Example 5; SEQ ID NO 20; 197pp; Japanese.  
XX  
CC The invention relates to replicon RNA from genotype 2a of hepatitis C  
CC virus comprising a 5' untranslated region, a base sequence encoding NS3  
CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a  
CC 3' untranslated region. The invention also relates to a cell capable of  
CC reproducing the replicon involving transducing the replicon RNA to a  
CC cell, a method of producing a hepatitis C virus protein, a method of  
CC screening a substance that promotes or suppresses the reproduction of  
CC hepatitis C virus, involving culturing the replicon reproducing cell in  
CC the presence of a test substance, and detecting the reproduction of  
CC replicon RNA in the culture. Virucide. The replicon RNA is useful for  
CC producing a replicon reproduction cell and for increasing the  
CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype  
CC 2a. The cell and the replicon RNA are useful for producing a therapeutic  
CC agent or a diagnostic agent for hepatitis C virus infection, for  
CC producing a vaccine against hepatitis C virus infection and for screening  
CC a substance that promotes or suppresses the reproduction of hepatitis C  
CC virus. This sequence represents a PCR primer used in the scope of the  
CC invention.  
XX

SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| ||| |||  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 5  
ADZ75974  
ID ADZ75974 standard; DNA; 24 BP.  
XX  
AC ADZ75974;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Hepatitis C virus specific probe SEQ ID NO:3.  
XX

KW DNA detection; RNA detection; hepatitis C virus infection;  
KW antiinflammatory; hepatotropic; virucide; probe; ss.

XX  
OS Hepatitis C virus.  
OS Synthetic.

XX  
PN US2005100889-A1.

XX  
PD 12-MAY-2005.

XX  
PF 13-OCT-2004; 2004US-00964302.

XX  
PR 04-DEC-2001; 2001US-00011855.

XX  
PA (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.

XX  
PI Baumann R, Hamdan H, Lewinski M;  
XX  
DR WPI; 2005-345387/35.

XX

PT Detecting Hepatitis C virus (HCV) nucleic acids in a test sample, for  
PT diagnosing HCV infection, comprises using oligonucleotide primers and  
PT probes to amplify HCV and/or control nucleic acid sequences present in  
PT the sample.

XX

PS Claim 1; SEQ ID NO 3; 13pp; English.

XX

CC The invention relates to a method for detecting the presence or amount of  
CC Hepatitis C virus (HCV) nucleic acids in a test sample. The method  
CC comprises: (a) introducing lambda phage-HCV nucleic acid hybrids into the  
CC test sample; (b) reverse transcribing and amplifying: (i) HCV nucleic  
CC acid if present in the sample and using a pair of oligonucleotide primers  
CC having the sequences set forth in ADZ75972 and ADZ75973, to generate HCV  
CC amplicons; and (ii) lambda phage-HCV hybrid nucleic acid using a pair of  
CC oligonucleotide primers having the sequences set forth in ADZ75972 and  
CC ADZ75973, to generate a lambda phage-HCV hybrid amplicons; (c)  
CC hybridizing the HCV amplicons with an oligonucleotide probe comprising  
CC the 24 bp sequence of ADZ75974 in the presence of an enzyme that cleaves  
CC the probe when the probe hybridizes to the HCV nucleic acids, where the  
CC probe is conjugated to a first detectable label that generates a  
detectable signal upon the cleavage; (d) hybridizing the lambda phage-HCV  
CC hybrid amplicons to a control oligonucleotide probe in the presence of an  
CC enzyme that cleaves the control oligonucleotide probe when the control  
CC probe hybridizes to the lambda phage-HCV hybrid amplicons, where the  
CC control probe is conjugated to a second detectable label that generates a  
detectable signal upon the cleavage; and (e) detecting a signal from the  
CC first and second detectable labels, where the signal from the first  
CC detectable label indicates the presence or amount of HCV nucleic acids in  
CC the test sample. Also described is a composition of one or more  
CC substantially purified oligonucleotides comprising the nucleotide  
CC sequences mentioned in the specification, and a kit comprising materials  
CC for performing the new method. The method and composition are useful for  
CC diagnosing HCV infection or for qualitatively and quantitatively  
CC detecting hepatitis C viral nucleic acids in a test sample. The present  
CC sequence represents an HCV specific probe which is used in an example  
CC from the present invention.

XX

SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| | | | | | | | | | | | | | | | | | | |  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 6

ADZ75978

ID ADZ75978 standard; DNA; 24 BP.

XX

AC ADZ75978;

XX

DT 14-JUL-2005 (first entry)

XX

DE Hepatitis C virus specific probe SEQ ID NO:7.

XX

KW DNA detection; RNA detection; hepatitis C virus infection;  
KW antiinflammatory; hepatotropic; virucide; probe; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

FH Key Location/Qualifiers  
FT misc\_binding 1  
FT /\*tag= a  
FT /bound\_moiety= "2'-chloro-7'-phenyl-1-4-dichloro-6-  
FT carboxyfluorescein (VIC)"  
FT misc\_binding 24  
FT /\*tag= b  
FT /bound\_moiety= "6-carboxytetramethylrhodamine (TAMRA)"  
XX  
PN US2005100889-A1.  
XX  
PD 12-MAY-2005.  
XX  
PF 13-OCT-2004; 2004US-00964302.  
XX  
PR 04-DEC-2001; 2001US-00011855.  
XX  
PA (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.  
XX  
PI Baumann R, Hamdan H, Lewinski M;  
XX  
DR WPI; 2005-345387/35.  
XX  
PT Detecting Hepatitis C virus (HCV) nucleic acids in a test sample, for  
PT diagnosing HCV infection, comprises using oligonucleotide primers and  
PT probes to amplify HCV and/or control nucleic acid sequences present in  
PT the sample.  
XX  
PS Example 2; SEQ ID NO 7; 13pp; English.  
XX  
CC The invention relates to a method for detecting the presence or amount of  
CC Hepatitis C virus (HCV) nucleic acids in a test sample. The method  
CC comprises: (a) introducing lambda phage-HCV nucleic acid hybrids into the  
CC test sample; (b) reverse transcribing and amplifying: (i) HCV nucleic  
CC acid if present in the sample and using a pair of oligonucleotide primers  
CC having the sequences set forth in ADZ75972 and ADZ75973, to generate HCV  
CC amplicons; and (ii) lambda phage-HCV hybrid nucleic acid using a pair of  
CC oligonucleotide primers having the sequences set forth in ADZ75972 and  
CC ADZ75973, to generate a lambda phage-HCV hybrid amplicons; (c)  
CC hybridizing the HCV amplicons with an oligonucleotide probe comprising  
CC the 24 bp sequence of ADZ75974 in the presence of an enzyme that cleaves  
CC the probe when the probe hybridizes to the HCV nucleic acids, where the  
CC probe is conjugated to a first detectable label that generates a  
CC detectable signal upon the cleavage; (d) hybridizing the lambda phage-HCV  
CC hybrid amplicons to a control oligonucleotide probe in the presence of an  
CC enzyme that cleaves the control oligonucleotide probe when the control  
CC probe hybridizes to the lambda phage-HCV hybrid amplicons, where the  
CC control probe is conjugated to a second detectable label that generates a  
CC detectable signal upon the cleavage; and (e) detecting a signal from the  
CC first and second detectable labels, where the signal from the first  
CC detectable label indicates the presence or amount of HCV nucleic acids in  
CC the test sample. Also described is a composition of one or more  
CC substantially purified oligonucleotides comprising the nucleotide  
CC sequences mentioned in the specification, and a kit comprising materials  
CC for performing the new method. The method and composition are useful for  
CC diagnosing HCV infection or for qualitatively and quantitatively  
CC detecting hepatitis C viral nucleic acids in a test sample. The present  
CC sequence represents an HCV specific probe which is used in an example  
CC from the present invention.  
XX  
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.059;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 7  
AAQ64955/c  
ID AAQ64955 standard; DNA; 27 BP.  
XX  
AC AAQ64955;  
XX  
DT 19-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KW inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 82; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 31  
CC bases from C at position 150 to G at position 180 of AAQ64913 and which  
CC contains at least 6 bases from C at position 175 to G at position 180.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 27 BP; 5 A; 11 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
Db 25 CCGGGAGAGCCATAGTGGTCTGCG 2

RESULT 8  
AAQ64950/c  
ID AAQ64950 standard; DNA; 30 BP.  
XX

AC AAQ64950;  
XX  
DT 19-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 80; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 31  
CC bases from C at position 150 to G at position 180 of AAQ64913 and which  
CC contains at least 6 bases from C at position 151 to C at position 156.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 30 BP; 5 A; 11 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| |||  
Db 25 CCGGGAGAGCCATAGTGGTCTGCG 2

RESULT 9  
AAX37631  
ID AAX37631 standard; DNA; 37 BP.  
XX  
AC AAX37631;  
XX  
DT 08-JUL-1999 (first entry)  
XX  
DE HCV detecting primer #1.  
XX  
KW Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;  
fluorescence resonance energy transfer; ss:  
XX  
OS Synthetic.  
OS Hepatitis C virus; Virus.

XX  
PN JP11103899-A.  
XX  
PD 20-APR-1999.  
XX  
PF 30-SEP-1997; 97JP-00283042.  
XX  
PR 30-SEP-1997; 97JP-00283042.  
XX  
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.  
PA (SRSL-) SRL KK.  
XX  
DR WPI; 1999-305862/26.

XX  
PT Measurement of HCV gene using real time detecting PCR and primer and  
PT - is highly sensitive.

XX  
PS Claim 1; Page 6; 8pp; Japanese.  
XX

CC This invention describes a method for the measurement of an HCV gene by a  
CC real time detecting PCR. The invention also describes a method where a  
CC reporter fluorescent colour and a quencher fluorescent colour are  
CC combined to an oligonucleotide and the fluorescence of the reporter  
CC fluorescent colour is controlled by fluorescence resonance energy  
CC transfer. The method can measure HCV exactly with high sensitivity  
XX

SQ Sequence 37 BP; 6 A; 15 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| |||  
Db 10 CCGGGAGAGCCATAGTGGTCTGCG 33

RESULT 10  
AAA52575  
ID AAA52575 standard; DNA; 50 BP.  
XX  
AC AAA52575;  
XX  
DT 27-SEP-2000 (first entry)  
XX  
DE HCV RNA promoter primer, SEQ ID NO:13.  
XX  
KW Oligonucleotide; HCV genomic RNA; detection; amplification;  
KW reverse transcription inhibition; translation inhibition; antiviral;  
KW gene therapy; sense; promoter primer; reverse transcription-PCR;  
KW RT-PCR primer; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN EP1002878-A2.  
XX  
PD 24-MAY-2000.  
XX  
PF 18-NOV-1999; 99EP-00122092.  
XX  
PR 19-NOV-1998; 98JP-00329874.  
XX  
PA (TOYJ ) TOSOH CORP.  
XX

PI Toshiki T, Takahiko I, Juichi S;  
XX  
DR WPI; 2000-352431/31.  
XX  
PT Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as  
PT reagents for gene diagnosis involving cleavage, amplification and  
PT detection of RNA and as an inhibitory drugs.  
XX  
PS Example 5; Page 15; 21pp; English.

CC The invention relates to single-stranded antisense oligodeoxynucleotides  
CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus  
CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)  
CC corresponding to sites on the HCV genome. The oligonucleotides are useful  
CC as primers in RT-PCR (reverse transcription-PCR) and the sense  
CC oligonucleotides may also be used as promoter primers. The antisense  
CC oligonucleotides may be used to inhibit translation or reverse  
CC transcription of HCV RNA and may be used as probes for detection of HCV  
CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving  
CC moiety to target single-stranded RNA cleavage or RNA heteroduplex  
CC cleavage. The invention also encompasses methods of identifying and  
CC preparing single-stranded oligodeoxynucleotides which bind to target  
CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents  
CC for genetic diagnosis involving cleavage, amplification and detection of  
CC HCV RNA (as primers and probes), and as inhibitors of reverse  
CC transcription or translation of HCV RNA. Sequences AAA42573-A52576  
CC represent HCV RNA promoter primers used in an exemplification of the  
CC invention

XX  
SQ Sequence 50 BP; 15 A; 9 C; 15 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| |||  
Db 26 CCGGGAGAGCCATAGTGGTCTGCG 49

RESULT 11  
AAQ98103/c  
ID AAQ98103 standard; DNA; 53 BP.  
XX  
AC AAQ98103;  
XX  
DT 05-FEB-1996 (first entry)  
XX  
DE Label extender probe used in an improved sandwich hybridisation assay.  
XX  
KW Probe; nucleotide; solution phase sandwich hybridisation assay;  
KW competitive; analyte binding sequence; background signal reduction; ss.  
XX  
OS Synthetic.  
XX  
PN WO9516055-A1.  
XX  
PD 15-JUN-1995.  
XX  
PF 07-DEC-1994; 94WO-US014119.  
XX  
PR 08-DEC-1993; 93US-00164388.  
XX  
PA (CHIR ) CHIRON CORP.

XX  
PI Urdea MS, Fultz T, Warner BD, Collins M;  
XX  
DR WPI; 1995-224335/29.  
XX  
PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with  
PT capture extender molecules or competitive oligo:nucleotide(s) to minimise  
PT background signal, increasing sensitivity and selectivity.  
XX  
PS Example 1; Page 33; 86pp; English.  
XX  
CC AAQ98100-Q98105 are label extender probes (LEs) used in a variation of a  
CC new improved method of a solution phase sandwich hybridisation assay in  
CC which LEs are used with a capture probe (CP). One label extender probe  
CC binds the target DNA and another binds to a labelled probe (LP). The new  
CC method minimises background signals (caused by non-specific  
CC hybridisation), this improves both sensitivity and selectivity of the  
CC assay without increasing cost or time  
XX  
SQ Sequence 53 BP; 9 A; 15 C; 20 G; 9 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 24; DB 2; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
|||  
Db 44 CCGGGAGAGCCATAGTGGTCTGCG 21  
  
RESULT 12  
AAT11268/c  
ID AAT11268 standard; RNA; 70 BP.  
XX  
AC AAT11268;  
XX  
DT 26-JUN-1996 (first entry)  
XX  
DE Hepatitis C virus partial 5'-UTR antisense RNA AS3.  
XX  
KW Antisense; therapy; complementary; HCV; 5'-untranslated region;  
KW hepatitis C virus; inhibition; infection; treatment; stem-loop;  
KW clone 2-1; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN JP07303485-A.  
XX  
PD 21-NOV-1995.  
XX  
PF 13-MAY-1994; 94JP-00124609.  
XX  
PR 13-MAY-1994; 94JP-00124609.  
XX  
PA (TOFU ) TONEN CORP.  
XX  
DR WPI; 1996-035187/04.  
XX  
PT Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene  
PT expression in vivo for treatment of HCV infection.  
XX  
PS Claim 2; Page 9; 12pp; Japanese.  
XX  
CC The present sequence is a specifically claimed example of RNA that is

CC complementary (i.e. antisense) to part of the 5'-untranslated region of  
CC the hepatitis C virus genome sequence contained in clone 2-1. The 5'-UTR  
CC includes several stem-loop sequences. The antisense RNA is useful for  
CC inhibiting expression of HCV structural genes and thereby inhibiting  
CC viral replication in vivo. The antisense therapy can be used in addition  
CC to conventional interferon treatment of HCV infections

XX

SQ Sequence 70 BP; 10 A; 21 C; 25 G; 0 T; 14 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.069;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| |||  
Db 51 CCGGGAGAGCCATAGTGGTCTGCG 28

RESULT 13

AEB94147/c

ID AEB94147 standard; DNA; 75 BP.

XX

AC AEB94147;

XX

DT 06-OCT-2005 (first entry)

XX

DE Nucleic acid detection method target sequence LTar-HCV.

XX

KW ss; probe; microorganism detection; DNA detection; RNA detection.

XX

OS Hepatitis C virus.

XX

PN WO2005071401-A2.

XX

PD 04-AUG-2005.

XX

PF 14-JAN-2005; 2005WO-US001378.

XX

PR 15-JAN-2004; 2004US-0536978P.

XX

PA (CHIR ) CHIRON CORP.

XX

PI Shyamala V, Nguyen SH;

XX

DR WPI; 2005-564246/57.

XX

PT Detecting a nucleic acid target sequence comprises contacting the sample  
PT with a capture probe conjugate, a reporter probe and a detectable  
PT reporter moiety.

XX

PS Example 1; SEQ ID NO 22; 42pp; English.

XX

CC The invention relates to a method of detecting a nucleic acid target  
CC sequence in a sample comprising contacting the sample with a capture  
CC probe conjugate, a reporter probe and a detectable reporter moiety. The  
CC method comprises: (i) contacting the sample with a capture probe  
CC conjugate, a reporter probe and a detectable reporter moiety, under  
CC conditions allowing formation of a complex including the nucleic acid  
CC target sequence, if present, the capture probe conjugate, the reporter  
CC probe and the detectable reporter moiety, where the capture probe  
CC conjugate and the reporter probe each comprise an oligonucleotide that is  
CC capable of specifically hybridizing to the nucleic acid target sequence  
CC and where the capture probe conjugate and the reporter probe do not  
CC hybridize to the same or overlapping regions of the nucleic acid target

CC sequence. The capture probe conjugate comprises a substrate having a  
CC distinguishable spectral signal signature that uniquely identifies the  
CC capture probe conjugate, where the reporter probe comprises one member of  
CC a binding pair and the detectable reporter moiety comprises the other  
CC member of the binding pair, and where the detectable reporter moiety  
CC comprises a detectable label; and (ii) detecting a signal from the  
CC capture probe conjugate substrate and the detectable reporter moiety  
CC label individually from each complex so formed. Also included is a kit  
CC for a multiplex assay for detecting the presence of nucleic acid target  
CC sequences in a sample, comprising: capture probe conjugates, reporter  
CC probes and a detectable reporter moiety, where each member of the capture  
CC probe conjugates is specific for one member of the target sequences (the  
CC specific capture probe conjugate) and each member of the reporter probes  
CC is specific for one member of the target sequences (the specific reporter  
CC probe). The nucleic acid target sequence is a sequence from a pathogen  
CC nucleic acid, where the pathogen is a virus selected from HIV, HBV, HCV,  
CC HAV, parvovirus B19, West Nile Virus, hantavirus or SARS. The method and  
CC kit are useful for detecting a nucleic acid target sequence in a sample.  
CC The present sequence represents a nucleic acid detection method target  
CC sequence.

XX

SQ Sequence 75 BP; 14 A; 24 C; 23 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 75;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| ||| |||  
Db 27 CCGGGAGAGCCATAGTGGTCTGCG 4

RESULT 14

ADJ53747

ID ADJ53747 standard; DNA; 86 BP.

XX

AC ADJ53747;

XX

DT 06-MAY-2004 (first entry)

XX

DE HBV specific molecular beacon target #16.

XX

KW ss; capture oligonucleotide; HBV; HIV-1; HCV; donated blood screening.

XX

OS Hepatitis B virus.

XX

PN WO2003106714-A1.

XX

PD 24-DEC-2003.

XX

PF 13-JUN-2003; 2003WO-US018993.

XX

PR 14-JUN-2002; 2002US-0389393P.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Linnen JM, Kolk DP, Dockter JM, Getman DK, Yoshimura T;

PI Ho-Sing-Loy M, Stringfellow LA;

XX

DR WPI; 2004-082210/08.

XX

PT Capture oligonucleotide composition useful for detection of hepatitis B  
PT virus (HBV), comprising polynucleotide having HBV-complementary sequence  
PT which is immobilized on solid support.

XX  
PS Example 10; SEQ ID NO 141; 112pp; English.  
XX  
CC The invention relates to a capture oligonucleotide composition comprising  
CC an hepatitis B virus (HBV)-complementary sequence polynucleotide  
CC immobilised to a solid support. The composition is useful for detecting  
CC nucleic acids of HBV and/or HIV-1 and/or HCV in biological sample such as  
CC blood, serum, plasma or other body fluid or tissue to be tested. The  
CC composition can be used either in diagnostic application or for screening  
CC donated blood and that products or other tissues that may contain  
CC infectious particles. The composition facilitates detection of very low  
CC levels of HBV nucleic acids. The composition allows selective detection  
CC of nucleic acids of HBV and/or HIV and/or HCV. The present sequence is  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 86 BP; 17 A; 26 C; 27 G; 16 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 24; DB 12; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.071;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
||| ||| ||| ||| ||| ||| |||  
Db 38 CCGGGAGAGCCATAGTGGTCTGCG 61  
  
RESULT 15  
AAC92379  
ID AAC92379 standard; RNA; 102 BP.  
XX  
AC AAC92379;  
XX  
DT 26-MAR-2001 (first entry)  
XX  
DE HCV-RNA WQ-RNA nucleotide sequence SEQ ID NO:7.  
XX  
KW Amplification; analysis; RNA transcription; RNA polymerase; detection;  
KW bacterium; virus; foodstuff; soil; environmental water; seawater;  
KW house dust; ss.  
XX  
OS Synthetic.  
XX  
PN WO200075371-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 05-JUN-2000; 2000WO-JP003647.  
XX  
PR 04-JUN-1999; 99JP-00157653.  
XX  
PA (TOYJ ) TOSOH CORP.  
XX  
PI Ishizuka T, Ishiguro T, Saitoh J, Sakai T;  
XX  
DR WPI; 2001-061738/07.  
XX  
PT Potentiated method for amplification of nucleic acids for detection in  
PT biological samples.  
XX  
PS Example 3; Page 38; 42pp; Japanese.  
XX  
CC The present invention describes a method for amplifying a specific RNA  
CC from a sample. The method comprises generating from the template RNA in  
CC the sample a two-stranded DNA, which contains sequences complementary to

CC and homologous with the RNA sequence, and a transcription promoter. RNA  
CC is transcribed from the two-stranded DNA using an RNA polymerase, in a  
CC reaction mixture comprising inosine triphosphate (ITP), Adenosine  
CC triphosphate (ATP), uridine triphosphate (UTP), cytidine triphosphate  
CC (CTP) and guanosine triphosphate (GTP), and the reaction cycle is  
CC repeated as necessary. The method can be used for the detection and assay  
CC of specific RNA sequences, such as those occurring in bacteria and  
CC viruses, in samples such as foodstuffs, soil, environmental waters,  
CC seawater and house dust. The addition of ITP increases the efficiency of  
CC the amplification reaction. The present sequence represents an  
CC oligonucleotide used in an example from the present invention, for the  
CC exemplification of the method of the invention

XX

SQ Sequence 102 BP; 23 A; 29 C; 25 G; 0 T; 25 U; 0 Other;

Query Match 100.0%; Score 24; DB 4; Length 102;  
Best Local Similarity 83.3%; Pred. No. 0.073;  
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24  
|||:|||||:||:||:||:|||  
Db 13 CCGGGAGAGCCAUAGUGGUCUGCG 36

Search completed: May 7, 2006, 06:32:34

Job time : 127.92 secs

SCORE 1.3 BuildDate: 12/06/2005

# SCORE Search Results Details for Application 10759

## Result us-10-759-514-6.rge.

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This page gives you Search Results detail for the Application 10759514 and Search Result us-10-759-514-start

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 06:16:29 ; Search time 512.074 Seconds  
(without alignments)  
2442.141 Million cell updates/sec

Title: US-10-759-514-6

Perfect score: 22

Sequence: 1 ttggcaacagtggcatgcaccc 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_in:  
3: gb\_env:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pr:  
9: gb\_ro:  
10: gb\_sts:  
11: gb\_sy:  
12: gb\_un:  
13: gb\_vi:  
14: gb\_htg:  
15: gb\_pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

%

Result      Query

No.	Score	Match Length	DB	ID	Description
c 1	22	100.0	1337	13 AF059603	AF059603 Wheat rosette virus
c 2	22	100.0	5557	6 CQ830721	CQ830721 Sequence
c 3	22	100.0	5557	6 CQ832100	CQ832100 Sequence
c 4	22	100.0	48502	7 LAMCG	J02459 Bacteriophage
c 5	19.4	88.2	44139	2 AY190942	AY190942 Drosophil
c 6	18.8	85.5	30844	15 AC158186	AC158186 Selaginel
	18.8	85.5	104771	9 AL603830	AL603830 Mouse DNA
8	18.8	85.5	206431	14 AC161885	AC161885 Gallus gallus
9	18.8	85.5	244279	14 AC163712	AC163712 Gallus gallus
10	18.8	85.5	248883	14 AC098544	AC098544 Rattus norvegicus
11	18.8	85.5	259215	14 AC118088	AC118088 Rattus norvegicus
12	18.8	85.5	262976	14 AC120483	AC120483 Rattus norvegicus
c 13	18.8	85.5	264908	9 AC096627	AC096627 Mus musculus
14	18.4	83.6	110000	1 BA000023_21	Continuation (22 o)
15	18.4	83.6	110000	1 BA000023_22	Continuation (23 o)
16	18.4	83.6	145993	8 AC098972	AC098972 Homo sapiens
17	18.4	83.6	167304	9 AL928678	AL928678 Mouse DNA
c 18	18.4	83.6	169111	14 CR954168	CR954168 Danio rerio
19	18.4	83.6	197839	9 AL845466	AL845466 Mouse DNA
20	18.4	83.6	207127	14 AC069496	AC069496 Homo sapiens
c 21	18.4	83.6	213005	8 AP005059	AP005059 Homo sapiens
22	18.4	83.6	220618	14 AC131892	AC131892 Atelerix
c 23	18.4	83.6	237739	14 AC134520	AC134520 Atelerix
24	17.8	80.9	905	10 BV576244	BV576244 G591P6073
c 25	17.8	80.9	32931	15 AC158190	AC158190 Selaginel
26	17.8	80.9	37165	15 AC158184	AC158184 Selaginel
27	17.8	80.9	39857	8 AC002522	AC002522 Homo sapiens
28	17.8	80.9	44873	8 AC004461	AC004461 Homo sapiens
29	17.8	80.9	59030	5 BX324184	BX324184 Zebrafish
30	17.8	80.9	97351	8 AC015853	AC015853 Homo sapiens
31	17.8	80.9	108400	8 HUMDGCRCEN	L77570 Homo sapiens
c 32	17.8	80.9	110000	1 BA000019_08	Continuation (9 o)
33	17.8	80.9	110000	15 CR382131_32	Continuation (33 o)
34	17.8	80.9	114540	8 AC107426	AC107426 Homo sapiens
35	17.8	80.9	125630	14 AC090650	AC090650 Arabidopsis thaliana
c 36	17.8	80.9	149939	5 AL935281	AL935281 Zebrafish
c 37	17.8	80.9	153284	8 AC078925	AC078925 Homo sapiens
c 38	17.8	80.9	157327	14 CR450752	CR450752 Danio rerio
39	17.8	80.9	157904	8 AC108486	AC108486 Homo sapiens
40	17.8	80.9	159868	8 AC122129	AC122129 Homo sapiens
c 41	17.8	80.9	159876	8 HS253P07	AL354000 Homo from
c 42	17.8	80.9	159994	8 AC157498	AC157498 Pan troglodytes
c 43	17.8	80.9	160256	5 BX950187	BX950187 Zebrafish
44	17.8	80.9	160583	14 AC154944	AC154944 Monodelphis domestica
45	17.8	80.9	169665	14 AC144566	AC144566 Homo sapiens

## ALIGNMENTS

RESULT 1  
AF059603/c  
LOCUS AF059603 1337 bp mRNA linear VRL 30-JAN-2000  
DEFINITION Wheat rosette stunt virus nucleocapsid protein (N) mRNA, partial cds.  
ACCESSION AF059603  
VERSION AF059603.1 GI:6815246  
KEYWORDS .  
SOURCE Wheat rosette stunt virus  
ORGANISM Wheat rosette stunt virus  
Viruses; ssRNA negative-strand viruses; Mononegavirales;  
Rhabdoviridae; unclassified Rhabdoviridae.

REFERENCE 1 (bases 1 to 1337)  
 AUTHORS Gong, Z.X.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-APR-1998) Virology Laboratory, Shanghai Institute of Biochemistry, Chinese Academy of Science, 320 Yue Yang Rd., Shanghai 200031, P.R. China  
 FEATURES Location/Qualifiers  
 source 1. .1337  
   /organism="Wheat rosette stunt virus"  
   /mol\_type="mRNA"  
   /db\_xref="taxon:75890"  
 gene <1. .1337  
   /gene="N"  
 CDS <1. .1209  
   /gene="N"  
   /codon\_start=1  
   /product="nucleocapsid protein"  
   /protein\_id="AAF28467.1"  
   /db\_xref="GI:6815247"  
   /translation="TFTKGDAERWVSTTKASDASAFLEVEGNSMTAPNGSKPSLAVI VHLSSSVEVIFGLGLSSSFRRLSICFRNYFIVILYHAYDNLLMSNLLILNKLFSLWLHQI KSRMMLAKSHRHPLDCLFVCQESYYTFCHRLLLRHVIIRNLAYRPIVFLIYKVD DTVLRCTGDSMILRHIVVHRIYIYIIICINRVACSATVAHRRYGRARRHVVCRNVVR LAGELPIVRLVNLDFQLLPILHIFCMREFVPPPTDHLSLYATVPRLLCAGATLQTSFSV HATVANDLPRNWLASYYRFCCKNSPPHIKSIRSLPISVVVISIFIIFMIPRKNLPSLLAR IQYSFPIIGKSFKSIIGFRFASINSDCSCRKRCGRTIFPYNFYERVSLSNHTQVLPC LQTIPVSNIK"

#### ORIGIN

Query Match 100.0%; Score 22; DB 13; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TTGGCAACAGTGGCATGCACCG 22  
   |||||||||||||||||||||||  
 Db 845 TTGGCAACAGTGGCATGCACCG 824

#### RESULT 2

CQ830721/c  
 LOCUS CQ830721 5557 bp DNA linear PAT 12-JUL-2004  
 DEFINITION Sequence 24 from Patent WO2004055215.  
 ACCESSION CQ830721  
 VERSION CQ830721.1 GI:50251007  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
   other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Otte, A.P. and van Blokland, H.J.  
 TITLE A method for improving protein production  
 JOURNAL Patent: WO 2004055215-A 24 01-JUL-2004;  
   Chromagenics B.V. (NL)  
 FEATURES Location/Qualifiers  
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DEFINITION Sequence 9 from Patent WO2004056986.  
ACCESSION CQ832100  
VERSION CQ832100.1 GI:50831814  
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ORGANISM Bacteriophage lambda  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
Lambda-like viruses.  
REFERENCE 1  
AUTHORS Otte, A.P., Kwaks, T.H. and Sewalt, R.G.  
TITLE Means and methods for producing a protein through chromatin openers  
that are capable of rendering chromatin more accessible to  
transcription factors  
JOURNAL Patent: WO 2004056986-A 9 08-JUL-2004;  
Chromagenics B.V. (NL)  
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DEFINITION Bacteriophage lambda, complete genome.  
ACCESSION J02459 M17233 M24325 V00636 X00906  
VERSION J02459.1 GI:215104  
KEYWORDS DNA-binding protein; circular; coat protein; complete genome;  
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SOURCE Bacteriophage lambda  
ORGANISM Bacteriophage lambda  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
Lambda-like viruses.  
REFERENCE 2 (bases 1 to 12)  
AUTHORS Wu, R. and Taylor, E.  
TITLE Nucleotide sequence analysis of DNA. II. Complete nucleotide  
sequence of the cohesive ends of bacteriophage lambda DNA  
JOURNAL J. Mol. Biol. 57 (3), 491-511 (1971)  
PUBMED 4931680  
REFERENCE 3 (bases 45493 to 45963)  
AUTHORS Imada, M. and Tsugita, A.  
TITLE Amino acid sequence of lambda phage endolysin  
JOURNAL Nature New Biol. 233, 230-231 (1971)  
REFERENCE 4 (sites)  
AUTHORS Weigel, P.H., Englund, P.T., Murray, K. and Old, R.W.

TITLE The 3'-terminal nucleotide sequences of bacteriophage lambda DNA  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 70 (4), 1151-1155 (1973)  
 PUBMED 4515613  
 REFERENCE 5 (bases 38597 to 38672)  
 AUTHORS Dahlberg,J.E. and Blattner,F.R.  
 TITLE In vitro transcription products of lambda DNA: Nucleotide sequences and regulatory sites  
 JOURNAL (in) Fox,C.F. and Robinson,W.S. (Eds.); VIRUS RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544; Academic Press, New York (1973)  
 REFERENCE 6 (bases 37945 to 38027)  
 AUTHORS Maniatis,T., Ptashne,M., Backman,K., Kield,D., Flashman,S., Jeffrey,A. and Maurer,R.  
 TITLE Recognition sequences of repressor and polymerase in the operators of bacteriophage lambda  
 JOURNAL Cell 5 (2), 109-113 (1975)  
 PUBMED 1095210  
 REFERENCE 7 (bases 35583 to 35600)  
 AUTHORS Kleid,D.G., Agarwal,K.L. and Khorana,H.G.  
 TITLE The nucleotide sequence in the promoter region of the gene N in bacteriophage lambda  
 JOURNAL J. Biol. Chem. 250 (14), 5574-5582 (1975)  
 PUBMED 167018  
 REFERENCE 8 (bases 35434 to 35618)  
 AUTHORS Dahlberg,J.E. and Blattner,F.R.  
 TITLE Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda  
 JOURNAL Nucleic Acids Res. 2 (9), 1441-1458 (1975)  
 PUBMED 1178525  
 REFERENCE 9 (bases 37945 to 38018)  
 AUTHORS Maniatis,T., Jeffrey,A. and Kleid,D.G.  
 TITLE Nucleotide sequence of the rightward operator of phage lambda  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (3), 1184-1188 (1975)  
 PUBMED 1055375  
 REFERENCE 10 (bases 44588 to 44773)  
 AUTHORS Sklar,J., Yot,P. and Weissman,S.M.  
 TITLE Determination of genes, restriction sites, and DNA sequences surrounding the 6S RNA template of bacteriophage lambda  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (5), 1817-1821 (1975)  
 PUBMED 1098044  
 REFERENCE 11 (bases 37905 to 37989)  
 AUTHORS Walz,,A., Pirrotta,V. and Ineichen,K.  
 TITLE Lambda repressor regulates the switch between PR and Prm promoters  
 JOURNAL Nature 262 (5570), 665-669 (1976)  
 PUBMED 958438  
 REFERENCE 12 (bases 37946 to 38039)  
 AUTHORS Smith,G.R., Eisen,H., Reichardt,L. and Hedgepeth,J.  
 TITLE Deletions of lambda phage locating a prm mutation within the rightward operator  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 73 (3), 712-716 (1976)  
 PUBMED 1062780  
 REFERENCE 13 (bases 35578 to 35667; 37903 to 38027)  
 AUTHORS Ptashne,M., Backman,K., Humayun,M.Z., Jeffrey,A., Maurer,R., Meyer,B. and Sauer,R.T.  
 TITLE Autoregulation and function of a repressor in bacteriophage lambda  
 JOURNAL Science 194 (4261), 156-161 (1976)  
 PUBMED 959843  
 REFERENCE 14 (bases 35578 to 35667)  
 AUTHORS Humayun,Z., Jeffrey,A. and Ptashne,M.  
 TITLE Completed DNA sequences and organization of repressor-binding sites in the operators of phage lambda  
 JOURNAL J. Mol. Biol. 112 (2), 265-277 (1977)  
 PUBMED 875019  
 REFERENCE 15 (bases 38610 to 38732)

AUTHORS Scherer,G., Hobom,G. and Kossel,H.  
TITLE DNA base sequence of the po promoter region of phage lamdba  
JOURNAL Nature 265 (5590), 117-121 (1977)  
PUBMED 834253  
REFERENCE 16 (bases 38041 to 38241)  
AUTHORS Roberts,T.M., Shimatake,H., Brady,C. and Rosenberg,M.  
TITLE Sequence of Cro gene of bacteriophage lambda  
JOURNAL Nature 270 (5634), 274-275 (1977)  
PUBMED 593347  
REFERENCE 17 (bases 27616 to 28935)  
AUTHORS Davies,R.W., Schreier,P.H. and Buchel,D.E.  
TITLE Nucleotide sequence of the attachment site of coliphage lambda  
JOURNAL Nature 270 (5639), 757-760 (1977)  
PUBMED 593399  
REFERENCE 18 (bases 37206 to 37263; 37914 to 37970)  
AUTHORS Humayun,Z.  
TITLE DNA sequence at the end of the cI gene in bacteriophage lambda  
JOURNAL Nucleic Acids Res. 4 (7), 2137-2143 (1977)  
PUBMED 909767  
REFERENCE 19 (bases 27617 to 27934)  
AUTHORS Landy,A. and Ross,W.  
TITLE Viral integration and excision: structure of the lambda att sites  
JOURNAL Science 197 (4309), 1147-1160 (1977)  
PUBMED 331474  
REFERENCE 20 (bases 39062 to 39170)  
AUTHORS Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and Blattner,F.R.  
TITLE Physical structure of the replication origin of bacteriophage lambda  
JOURNAL Science 198 (4321), 1051-1056 (1977)  
PUBMED 929187  
REFERENCE 21 (bases 44467 to 44807)  
AUTHORS Sklar,J.L.  
TITLE Structure and function of two regions of DNA controlling the synthesis of prokaryotic RNAs  
JOURNAL Thesis (1977)  
REFERENCE 22 (sites)  
AUTHORS Adhya,S. and Gottesman,M.  
TITLE Control of transcription termination  
JOURNAL Annu. Rev. Biochem. 47, 967-996 (1978)  
PUBMED 354508  
REFERENCE 23 (bases 13 to 72; 48391 to 48502)  
AUTHORS Nichols,B.P. and Donelson,J.E.  
TITLE 178-Nucleotide sequence surrounding the cos site of bacteriophage lambda DNA  
JOURNAL J. Virol. 26 (2), 429-434 (1978)  
PUBMED 666898  
REFERENCE 24 (bases 37938 to 38016; 35589 to 35666)  
AUTHORS Flashman,S.M.  
TITLE Mutational analysis of the operators of bacteriophage lambda  
JOURNAL Mol. Gen. Genet. 166 (1), 61-73 (1978)  
PUBMED 368570  
REFERENCE 25 (bases 37990 to 38982)  
AUTHORS Schwarz,E., Scherer,G., Hobom,G. and Kossel,H.  
TITLE Nucleotide sequence of cro, cII and part of the O gene in phage lambda DNA  
JOURNAL Nature 272 (5652), 410-414 (1978)  
PUBMED 264238  
REFERENCE 26 (bases 38212 to 38362)  
AUTHORS Rosenberg,M., Court,D., Shimatake,H., Brady,C. and Wulff,D.L.  
TITLE The relationship between function and DNA sequence in an intercistronic regulatory region in phage lambda  
JOURNAL Nature 272 (5652), 414-423 (1978)  
PUBMED 634366

REFERENCE 27 (bases 37224 to 37940)  
 AUTHORS Sauer,R.T.  
 TITLE DNA sequence of the bacteriophage gama cI gene  
 JOURNAL Nature 276 (5685), 301-302 (1978)  
 PUBMED 714163  
 REFERENCE 28 (bases 38597 to 39688)  
 AUTHORS Scherer,G.  
 TITLE Nucleotide sequence of the O gene and of the origin of replication  
 in bacteriophage lambda DNA  
 JOURNAL Nucleic Acids Res. 5 (9), 3141-3156 (1978)  
 PUBMED 704348  
 REFERENCE 29 (bases 29711 to 29811; 31043 to 31058)  
 AUTHORS Davies,R.W., Schreier,P.H. and Buchel,D.E.  
 TITLE Determination of the endpoints of partial deletion mutants of the  
 attachment site of bacteriophage lambda by DNA sequencing  
 JOURNAL Nucleic Acids Res. 5 (9), 3209-3218 (1978)  
 PUBMED 704352  
 REFERENCE 30 (bases 21661 to 31129)  
 AUTHORS Hoess,R.H. and Landy,A.  
 TITLE Structure of the lambda att sites generated by int-dependent  
 deletions  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 75 (11), 5437-5441 (1978)  
 PUBMED 364480  
 REFERENCE 31 (bases 38453 to 38500)  
 AUTHORS Sprague,K.U., Faulds,D.H. and Smith,G.R.  
 TITLE A single base-pair change creates a Chi recombinational hotspot in  
 bacteriophage lambda  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 75 (12), 6182-6186 (1978)  
 PUBMED 282634  
 REFERENCE 32 (bases 27711 to 27826)  
 AUTHORS Ross,W., Landy,A., Kikuchi,Y. and Nash,H.  
 TITLE Interaction of int protein with specific sites on lambda att DNA  
 JOURNAL Cell 18 (2), 297-307 (1979)  
 PUBMED 159130  
 REFERENCE 33 (bases 38008 to 39328)  
 AUTHORS Moore,D.D., Denniston-Thompson,K., Kruger,K.E., Furth,M.E.,  
 Williams,B.G., Daniels,D.L. and Blattner,F.R.  
 TITLE Dissection and comparative anatomy of the origins of replication of  
 lambdoid phages  
 JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 155-163 (1979)  
 PUBMED 157834  
 REFERENCE 34 (bases 38470 to 39189)  
 AUTHORS Hobom,G., Grosschedl,R., Lusky,M., Scherer,G., Schwarz,E. and  
 Kossel,H.  
 TITLE Functional analysis of the replicator structure of lambdoid  
 bacteriophage DNAs  
 JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 165-178 (1979)  
 PUBMED 157835  
 REFERENCE 35 (bases 38453 to 38500)  
 AUTHORS Smith,G.R., Faulds,D.H. and Sprague,K.U.

Query Match 100.0%; Score 22; DB 7; Length 48502;  
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 ORGANISM Drosophila pseudoobscura  
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 Ephydrioidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 44139)  
 AUTHORS Bergman,C.M., Pfeiffer,B.D., Rincon-Limas,D.E., Hoskins,R.A.,  
 Gnrke,A., Mungall,C.J., Wang,A.M., Kronmiller,B., Pacleb,J.,  
 Park,S., Stapleton,M., Wan,K., George,R.A., de Jong,P.J., Botas,J.,  
 Rubin,G.M. and Celniker,S.E.  
 TITLE Assessing the impact of comparative genomic sequence data on the  
 functional annotation of the Drosophila genome  
 JOURNAL Genome Biol. 3 (12), research0086 (2002)  
 REMARK http://genomebiology.com/2002/3/12/research/0086  
 REFERENCE 2 (bases 1 to 44139)  
 AUTHORS Pfeiffer,B.D., Bergman,C.M., Gnrke,A., Hoskins,R.A., Moshrefi,A.,  
 Mungall,C.J., Pacleb,J., Wang,A.M., Park,S., Wan,K., George,R.A.,  
 Rubin,G.M. and Celniker,S.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-DEC-2002) Berkeley Drosophila Genome Project,  
 Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, Berkeley, CA  
 94720, USA  
 COMMENT Gene annotations are preliminary because they are based solely on  
 alignments of conceptually translated gene models to the  
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ORIGIN

Query Match 88.2%; Score 19.4; DB 2; Length 44139;  
Best Local Similarity 95.2%; Pred. No. 73;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 TGGCAACAGTGGCATGCACCG 22  
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Db 5482 TGGCAACAGTGCCATGCACCG 5462

RESULT 6

AC158186/c

LOCUS AC158186 30844 bp DNA linear PLN 26-MAY-2005  
DEFINITION Selaginella moellendorffii clone JGIASXY-5F17, complete sequence.  
ACCESSION AC158186  
VERSION AC158186.2 GI:66730719  
KEYWORDS HTG.  
SOURCE Selaginella moellendorffii  
ORGANISM Selaginella moellendorffii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;  
Selaginella.  
REFERENCE 1 (bases 1 to 30844)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 30844)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2005) Production Genomics Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA  
94598-1698, USA  
REFERENCE 3 (bases 1 to 30844)  
AUTHORS Stanford Human Genome Center.  
CONSRTM DOE Joint Genome Institute  
TITLE Direct Submission  
JOURNAL Submitted (26-MAY-2005) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
COMMENT On May 26, 2005 this sequence version replaced gi:60650325.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www-shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.  
FEATURES Location/Qualifiers  
source 1..30844  
/organism="Selaginella moellendorffii"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:88036"  
/clone="JGIASXY-5F17"

ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 30844;  
Best Local Similarity 90.9%; Pred. No. 1.5e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TTGGCAACAGTGGCATGCACCG 22  
||| ||| ||| |||  
Db 2812 TTGGCACCACTGGCATGCTCCG 2791

**RESULT 7**  
**AL603830**  
**LOCUS** AL603830 104771 bp DNA linear ROD 09-FEB-2005  
**DEFINITION** Mouse DNA sequence from clone RP23-467E19 on chromosome 11 Contains the Map2k3 gene for mitogen activated protein kinase kinase 3, the Gtlf3a gene for gene trap locus F3a, the Gtlf3b gene for gene trap locus F3b and two CpG islands, complete sequence.  
**ACCESSION** AL603830  
**VERSION** AL603830.7 GI:17017794  
**KEYWORDS** HTG; CpG island; Gtlf3a; Gtlf3b; kinase; Map2K3.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 104771)  
**AUTHORS** Clark,S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (04-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk  
Clone requests: clonerequest@sanger.ac.uk  
**COMMENT** On Nov 20, 2001 this sequence version replaced gi:16944205.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) -----  
Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: vega@sanger.ac.uk  
-----  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.  
RP23-467E19 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.  
For further details see <http://www.chori.org/bacpac/home.htm>  
**VECTOR:** pBACe3.6.  
**FEATURES** Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="11"  
/clone="RP23-467E19"  
/clone\_lib="RPCI-23"  
**gene** complement(join(36672. .37719,38280. .38325,39423. .39562, 42295. .42372,42712. .42839,44702. .44818,45877. .45996, 46219. .46332,47130. .47178,47537. .47603,57212. .57429))  
/gene="Map2k3"  
/locus\_tag="RP23-467E19.1-002"  
**gene** complement(join(36672. .37719,38280. .38325,39423. .39562,

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42295. . 42372,42712. . 42839,43921. . 43972,44702. . 44818,
45877. . 45996,46219. . 46332,47130. . 47178,47537. . 47603,
57212. . 57429))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-001"
complement(join(36672. . 37719,38280. . 38325,39423. . 39562,
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46219. . 46332,47130. . 47178,47537. . 47603,57212. . 57429))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-002"
/product="mitogen activated protein kinase kinase 3"
/note="match: cDNAs: BC007467.1"
mRNA complement(join(36672. . 37719,38280. . 38325,39423. . 39562,
42295. . 42372,42712. . 42839,43921. . 43972,44702. . 44818,
45877. . 45996,46219. . 46332,47130. . 47178,47537. . 47603,
57212. . 57429))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-002"
/product="mitogen activated protein kinase kinase 3"
/note="match: ESTs: AA008333.1 AA433619.1 AV238394.1
AW106586.1 AW539252.1 BB858602.1 BF234702.1 BI555968.1
BY019272.1 BY226967.1 BY685384.1 BY710384.1 CA569861.1
CB947897.1 CB951524.1 W78467.1
match: cDNAs: AK008141.1 AK011002.1 AK093838.1 BC032478.1
D87116.1 U66839.1"
CDS complement(join(37636. . 37719,38280. . 38325,39423. . 39562,
42295. . 42372,42712. . 42839,43921. . 43972,44702. . 44818,
45877. . 45996,46219. . 46332,47130. . 47178,47537. . 47603,
57212. . 57260))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-002"
/standard_name="OTTMUSP00000006687"
/note="match: proteins: O09110 P46734"
/codon_start=1
/product="mitogen activated protein kinase kinase 3"
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/db_xref="GI:56237940"
/db_xref="InterPro:IPR000719"
/db_xref="InterPro:IPR002290"
/db_xref="InterPro:IPR008271"
/db_xref="InterPro:IPR011009"
/translation="MESPAA$PPASLPQTGKSKRKDLRISCVSKPPVSNPTPPRNL
DSRTFITIGDRNFEVEADDLVTVTSELGRGAYGVVEKVRHAQSGTIMAVKRIRATVNTQ
EQKRLLMDLDINMRDVFYTVTFYGYALFREGDVWICMELMDTSLDKFYRKVLEKNMK
IPEDILGEIAVSIVRALEHLHSKLSVIHRDVVKPSNVLINKEGHVKMCDFGISGYLVDS
VAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSL GITMIEMAILRFPYESWGTPFQ
QLKQVVEEPSPSQLPADQFSPEFVDFTSQCLRKNPAERM$YLELMEHPFFTLHKT$KD
IAAFVKEILGEDS"
gene complement(join(37662. . 37719,38280. . 38821))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-006"
mRNA complement(join(37662. . 37719,38280. . 38821))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-006"
/product="mitogen activated protein kinase kinase 3"
/note="match: ESTs: BF467851.1"
gene complement(join(41892. . 42372,42712. . 42839,43921. . 43972,
44702. . 44818,45877. . 45996,46219. . 46332,47130. . 47178,
47537. . 47603,57212. . 57429))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-003"
mRNA complement(join(41892. . 42372,42712. . 42839,43921. . 43972,
44702. . 44818,45877. . 45996,46219. . 46332,47130. . 47178,
47537. . 47603,57212. . 57429))

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/locus_tag="RP23-467E19.1-003"
/product="mitogen activated protein kinase kinase 3"
/note="match: ESTs: BB538636.2 BY724665.1
match: cDNAs: AK053378.1"
gene complement(join(42712. .42839,43921. .43972,44702. .44818,
45877. .45996,46219. .46332,47083. .47178,47537. .47603))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-004"
complement(join(42712. .42839,43921. .43972,44702. .44818,
45877. .45996,46219. .46332,47083. .47178,47537. .47603))
/mRNA /gene="Map2k3"
/locus_tag="RP23-467E19.1-004"
/product="mitogen activated protein kinase kinase 3"
/note="match: ESTs: BI525531.1"
gene complement(join(47367. .47603,57212. .57429))
/gene="Map2k3"
/locus_tag="RP23-467E19.1-005"
complement(join(47367. .47603,57212. .57429))
/mRNA /gene="Map2k3"
/locus_tag="RP23-467E19.1-005"
/product="mitogen activated protein kinase kinase 3"
/note="match: ESTs: BB857429.1"
gene join(57616. .57917,67578. .68566)
/gene="Gtlf3a"
/locus_tag="RP23-467E19.2-001"
join(57616. .57917,67578. .68566)
/mRNA /gene="Gtlf3a"
/locus_tag="RP23-467E19.2-001"
/product="gene trap locus F3a"
/note="match: ESTs: AI466976.1 AV085862.1 AV092279.1
AV253865.2 AV279917.1 BF099931.1 BY357260.1 BY709130.1
BY709606.1 BY709640.1
match: cDNAs: AK009371.1 AK010055.1 AK010107.1 BC031537.1"
gene join(74733. .74800,82483. .82601,83362. .83529)
/gene="Gtlf3b"
/locus_tag="RP23-467E19.3-002"
join(74733. .74800,82483. .82601,83362. .83529)
/mRNA /gene="Gtlf3b"
/locus_tag="RP23-467E19.3-002"
/product="gene trap locus F3b"
/note="match: ESTs: BY176117.1 BY178036.1 BY190148.1"
gene join(75671. .75854,82483. .82601,83362. .87237)
/gene="Gtlf3b"
/locus_tag="RP23-467E19.3-001"
join(75671. .75854,82483. .82601,83362. .87237)
/mRNA /gene="Gtlf3b"
/locus_tag="RP23-467E19.3-001"
/product="gene trap locus F3b"
/note="match: ESTs: AI413349.1 AI425923.1 BE308889.1
BE996115.1 BU152631.1 BY177308.1 BY196792.1 BY198579.1
BY202343.1 BY203840.1 BY747733.1
match: cDNAs: AK004720.2 AK080453.1 BC034332.1 BC038816.1"
CDS join(75758. .75854,82483. .82601,83362. .83478)
/gene="Gtlf3b"
/locus_tag="RP23-467E19.3-002"
/standard_name="OTTMUSP00000006007"
/note="match: proteins: Q8N6N6 Q9DBW3"
/codon_start=1
/product="gene trap locus F3b"
/protein_id="CAI25795.1"
/db_xref="GI:56237941"
/translation="MAHATPPSALEQGGPIRVEHDRQRRQFSVRLNGCHDRAVLLYEV
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   /gene="Gtlf3b"  
   /locus\_tag="RP23-467E19.3-001"  
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   /gene="Gtlf3b"  
   /locus\_tag="RP23-467E19.3-001"

**ORIGIN**

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Query Match      85.5%; Score 18.8; DB 9; Length 104771;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TTGGCAACAGTGGCATGCACCG 22
        ||||||| | | | | | |
Db      6473 TTGGCAACAGTGCCATGCACAG 6494
  
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**RESULT 8**

**AC161885**

**LOCUS** AC161885 206431 bp DNA linear HTG 21-MAY-2005  
**DEFINITION** Gallus gallus chromosome UNKNOWN clone CH261-15B19, WORKING DRAFT  
SEQUENCE, 8 unordered pieces.  
**ACCESSION** AC161885  
**VERSION** AC161885.1 GI:66392501  
**KEYWORDS** HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
**SOURCE** Gallus gallus (chicken)  
**ORGANISM** Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
**REFERENCE** 1 (bases 1 to 206431)  
**AUTHORS** Wilson, R.K.  
**TITLE** The sequence of Gallus gallus clone  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 206431)  
**AUTHORS** Wilson, R.K.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-MAY-2005) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
**COMMENT**  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@watson.wustl.edu  
----- Project Information -----  
Center project name: J\_AA015B19  
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----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-primer ET; 0% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 203515 bases at least Q40  
Consensus quality: 204721 bases at least Q30  
Consensus quality: 205241 bases at least Q20  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.

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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*      1    3949: contig of 3949 bp in length
*    3950    4049: gap of unknown length
*    4050    9460: contig of 5411 bp in length
*    9461    9560: gap of unknown length
*    9561   20832: contig of 11272 bp in length
*   20833   20932: gap of unknown length
*   20933   37073: contig of 16141 bp in length
*   37074   37173: gap of unknown length
*   37174   56455: contig of 19282 bp in length
*   56456   56555: gap of unknown length
*   56556  100723: contig of 44168 bp in length
* 100724  100823: gap of unknown length
* 100824  155191: contig of 54368 bp in length
* 155192  155291: gap of unknown length
* 155292  206431: contig of 51140 bp in length.

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                  clone_end:T7
                  vector_side:right"
gap              3950. .4049
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4050. .9460
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9461. .9560
                  /estimated_length=unknown
misc_feature     9561. .20832
                  /note="assembly_name:Contig4"
gap              20833. .20932
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gap              56456. .56555
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gap              100724. .100823
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ORIGIN

Query Match 85.5%; Score 18.8; DB 14; Length 206431;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22

|| ||||||| |  
Db 26993 TTAGCAACAGTGGCATGCACAG 27014

RESULT 9

AC163712

LOCUS AC163712 244279 bp DNA linear HTG 13-JUN-2005  
DEFINITION Gallus gallus chromosome UNKNOWN clone CH261-29M9, WORKING DRAFT  
SEQUENCE, 32 unordered pieces.  
ACCESSION AC163712  
VERSION AC163712.1 GI:67515067  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 244279)  
AUTHORS Wilson, R.K.  
TITLE The sequence of Gallus gallus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 244279)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUN-2005) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: submissions@watson.wustl.edu

----- Project Information -----

Center project name: J\_AA029M09

----- Summary Statistics -----

Sequencing vector: M13; 0%

Sequencing vector: plasmid; 100%

Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 231430 bases at least Q40

Consensus quality: 235038 bases at least Q30

Consensus quality: 237275 bases at least Q20

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 32 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 1283: contig of 1283 bp in length  
\* 1284 1383: gap of unknown length  
\* 1384 2584: contig of 1201 bp in length  
\* 2585 2684: gap of unknown length  
\* 2685 3930: contig of 1246 bp in length  
\* 3931 4030: gap of unknown length  
\* 4031 5280: contig of 1250 bp in length  
\* 5281 5380: gap of unknown length  
\* 5381 7337: contig of 1957 bp in length  
\* 7338 7437: gap of unknown length  
\* 7438 9021: contig of 1584 bp in length

\* 9022 9121: gap of unknown length  
 \* 9122 11089: contig of 1968 bp in length  
 \* 11090 11189: gap of unknown length  
 \* 11190 13486: contig of 2297 bp in length  
 \* 13487 13586: gap of unknown length  
 \* 13587 15833: contig of 2247 bp in length  
 \* 15834 15933: gap of unknown length  
 \* 15934 17435: contig of 1502 bp in length  
 \* 17436 17535: gap of unknown length  
 \* 17536 19371: contig of 1836 bp in length  
 \* 19372 19471: gap of unknown length  
 \* 19472 22284: contig of 2813 bp in length  
 \* 22285 22384: gap of unknown length  
 \* 22385 25532: contig of 3148 bp in length  
 \* 25533 25632: gap of unknown length  
 \* 25633 30124: contig of 4492 bp in length  
 \* 30125 30224: gap of unknown length  
 \* 30225 33511: contig of 3287 bp in length  
 \* 33512 33611: gap of unknown length  
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 \* 36771 36870: gap of unknown length  
 \* 36871 42189: contig of 5319 bp in length  
 \* 42190 42289: gap of unknown length  
 \* 42290 46491: contig of 4202 bp in length  
 \* 46492 46591: gap of unknown length  
 \* 46592 50239: contig of 3648 bp in length  
 \* 50240 50339: gap of unknown length  
 \* 50340 54250: contig of 3911 bp in length  
 \* 54251 54350: gap of unknown length  
 \* 54351 58613: contig of 4263 bp in length  
 \* 58614 58713: gap of unknown length  
 \* 58714 67049: contig of 8336 bp in length  
 \* 67050 67149: gap of unknown length  
 \* 67150 74757: contig of 7608 bp in length  
 \* 74758 74857: gap of unknown length  
 \* 74858 82727: contig of 7870 bp in length  
 \* 82728 82827: gap of unknown length  
 \* 82828 93016: contig of 10189 bp in length  
 \* 93017 93116: gap of unknown length  
 \* 93117 105498: contig of 12382 bp in length  
 \* 105499 105598: gap of unknown length  
 \* 105599 119371: contig of 13773 bp in length  
 \* 119372 119471: gap of unknown length  
 \* 119472 132312: contig of 12841 bp in length  
 \* 132313 132412: gap of unknown length  
 \* 132413 154469: contig of 22057 bp in length  
 \* 154470 154569: gap of unknown length  
 \* 154570 175487: contig of 20918 bp in length  
 \* 175488 175587: gap of unknown length  
 \* 175588 197601: contig of 22014 bp in length  
 \* 197602 197701: gap of unknown length  
 \* 197702 244279: contig of 46578 bp in length.

FEATURES	Location/Qualifiers
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	/estimated_length=unknown
misc_feature	1384. .2584

/note="assembly\_name:Contig30"  
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misc\_feature  /estimated\_length=unknown  
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gap           3931. .4030  
misc\_feature  /estimated\_length=unknown  
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gap           /estimated\_length=unknown  
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              5381. .7337  
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              7438. .9021  
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              9022. .9121  
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Query Match          85.5%;  Score 18.8;  DB 14;  Length 244279;
Best Local Similarity 90.9%;  Pred. No. 1.3e+02;
Matches   20;  Conservative    0;  Mismatches    2;  Indels     0;  Gaps     0;

Qy      1 TTGGCAACAGTGGCATGCACCG 22
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RESULT 10  
AC098544

LOCUS AC098544 248883 bp DNA linear HTG 10-MAY-2003

DEFINITION Rattus norvegicus clone CH230-103A8, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 5 unordered pieces.

ACCESSION AC098544

VERSION AC098544.6 GI:30521653

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 248883)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
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Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 248883)  
AUTHORS Worley,K.C.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
REFERENCE 3 (bases 1 to 248883)  
AUTHORS Rat Genome Sequencing Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
COMMENT On May 10, 2003 this sequence version replaced gi:22855582.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GHJG  
Center clone name: CH230-103A8  
----- Summary Statistics  
Assembly program: Atlas 3.0;  
Consensus quality: 223541 bases at least Q40  
Consensus quality: 226408 bases at least Q30  
Consensus quality: 228553 bases at least Q20  
Estimated insert size: 235340; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*       1 242485: contig of 242485 bp in length  
\* 242486 242585: gap of unknown length  
\* 242586 243738: contig of 1153 bp in length  
\* 243739 243838: gap of unknown length  
\* 243839 245069: contig of 1231 bp in length  
\* 245070 245169: gap of unknown length  
\* 245170 246652: contig of 1483 bp in length  
\* 246653 246752: gap of unknown length  
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## FEATURES

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ORIGIN

Query Match 85.5%; Score 18.8; DB 14; Length 248883;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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## RESULT 11

AC118088

AC118088 259215 bp DNA linear HTG 19-NOV-2002

#### **DEFINITION** Battus n.

ACCESSION AC118088

VERSION AC118088.5 GT:25087858

KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT;

SOURCE *Rattus norvegicus* (Norway rat)

**ORGANISM** Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 259215)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H..

Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemech,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczek,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 259215)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 259215)
AUTHORS	Rat Genome Sequencing Consortium.
TITLE	Direct Submission
JOURNAL	Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Nov 19, 2002 this sequence version replaced gi:23265586. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas ( <a href="http://www.hgsc.bcm.tmc.edu/projects/rat/">http://www.hgsc.bcm.tmc.edu/projects/rat/</a> ). Each contig described

in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GUPO  
Center clone name: CH230-30B23  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 238249 bases at least Q40  
Consensus quality: 240765 bases at least Q30  
Consensus quality: 242460 bases at least Q20  
Estimated insert size: 245419; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 259215: contig of 259215 bp in length.

FEATURES  
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ORIGIN

Query Match 85.5%; Score 18.8; DB 14; Length 259215;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22  
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RESULT 12

AC120483

LOCUS AC120483 262976 bp DNA linear HTG 15-NOV-2002  
DEFINITION Rattus norvegicus clone CH230-13K13, WORKING DRAFT SEQUENCE, 2  
unordered pieces.  
ACCESSION AC120483  
VERSION AC120483.4 GI:25008120  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 262976)  
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
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Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,  
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,  
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,  
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,

Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,  
 Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,  
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
 Williams,G., Willson,R., Wleczik,R., Wooden,H., Worley,K.,  
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G. and Gibbs,R.A.

**TITLE** Direct Submission  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 262976)  
**AUTHORS** Worley,K.C.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (07-MAY-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
**REFERENCE** 3 (bases 1 to 262976)  
**AUTHORS** Rat Genome Sequencing Consortium.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (15-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
**COMMENT**  
 On Nov 15, 2002 this sequence version replaced gi:23265426.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GXNG  
 Center clone name: CH230-13K13  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 242345 bases at least Q40  
 Consensus quality: 245593 bases at least Q30  
 Consensus quality: 247807 bases at least Q20  
 Estimated insert size: 249832; sum-of-contigs estimation  
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 258816: contig of 258816 bp in length  
 \* 258817 258916: gap of unknown length  
 \* 258917 262976: contig of 4060 bp in length.

FEATURES Location/Qualifiers

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   /organism="Rattus norvegicus"  
   /mol\_type="genomic DNA"  
   /db\_xref="taxon:10116"  
   /clone="CH230-13K13"

misc\_feature 1. .1927  
   /note="wgs\_end\_extension  
   clone\_end:Sp6"

misc\_feature complement(5096. .5877)  
   /note="clone\_boundary  
   clone\_end:Sp6  
   site:  
   end\_sequence:BH274933"  
 137741. .139060

misc\_feature complement(256373. .257121)  
   /note="clone\_boundary  
   clone\_end:T7  
   site:  
   end\_sequence:BH274931"  
 257721. .258816

misc\_feature /note="wgs\_end\_extension  
   clone\_end:T7"  
 gap 258817. .258916  
   /estimated\_length=unknown

#### ORIGIN

Query Match                85.5%; Score 18.8; DB 14; Length 262976;  
 Best Local Similarity    90.9%; Pred. No. 1.3e+02;  
 Matches    20; Conservative    0; Mismatches    2; Indels    0; Gaps    0;

Qy                1 TTGGCAACAGTGGCATGCACCG 22  
                   ||||||| | | | | | | | | | |  
 Db                45102 TTGGCAACAGTGCCATGCACAG 45123

RESULT 13  
 AC096627/c

LOCUS                AC096627                264908 bp        DNA        linear      ROD 03-MAY-2003

DEFINITION        Mus musculus strain C57BL/6J clone rp23-77b23 map 11, complete sequence.

ACCESSION        AC096627

VERSION          AC096627.28    GI:30349025

KEYWORDS        HTG.

SOURCE            Mus musculus (house mouse)

ORGANISM        Mus musculus  
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
                   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
                   Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE        1 (bases 1 to 264908)

AUTHORS          Ni,Y., Song,L. and Roe,B.A.

TITLE             Mus musculus BAC Clone rp23-77b23

JOURNAL         Unpublished

REFERENCE        2 (bases 1 to 264908)

AUTHORS          Ni,Y., Song,L. and Roe,B.A.

TITLE             Direct Submission

JOURNAL         Submitted (19-SEP-2001) Department Of Chemistry And Biochemistry,  
                   The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
                   OK 73019, USA

REFERENCE        3 (bases 1 to 264908)

AUTHORS          Ni,Y., Song,L. and Roe,B.A.

TITLE             Direct Submission

JOURNAL         Submitted (02-MAY-2003) Department Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
REFERENCE 4 (bases 1 to 264908)  
AUTHORS Ni,Y., Song,L. and Roe,B.A.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAY-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT On May 3, 2003 this sequence version replaced gi:29423919.  
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Genome Center  
Center: Department Of Chemistry And Biochemistry  
The University Of Oklahoma  
Center code:UOKNOR  
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FEATURES Location/Qualifiers  
source 1. .264908  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/map="11"  
/clone="rp23-77b23"  
/clone\_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"

## ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 264908;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TTGGCACACAGTGGCATGCACCG 22  
||| ||| ||| ||| ||| ||| |||  
Db 172994 TTGGCACACAGTGCCATGCACAG 172973

## RESULT 14

BA000023\_21

## WPCOMMENT

Sequence split into 27 fragments LOCUS BA000023 Accession BA000023

Fragment Name	Begin	End
BA000023_00	1	110000
BA000023_01	100001	210000
BA000023_02	200001	310000
BA000023_03	300001	410000
BA000023_04	400001	510000
BA000023_05	500001	610000
BA000023_06	600001	710000
BA000023_07	700001	810000
BA000023_08	800001	910000
BA000023_09	900001	1010000
BA000023_10	1000001	1110000
BA000023_11	1100001	1210000
BA000023_12	1200001	1310000
BA000023_13	1300001	1410000
BA000023_14	1400001	1510000
BA000023_15	1500001	1610000
BA000023_16	1600001	1710000
BA000023_17	1700001	1810000
BA000023_18	1800001	1910000
BA000023_19	1900001	2010000
BA000023_20	2000001	2110000
BA000023_21	2100001	2210000
BA000023_22	2200001	2310000
BA000023_23	2300001	2410000
BA000023_24	2400001	2510000

BA000023\_25 2500001 2610000  
BA000023\_26 2600001 2694756

Continuation (22 of 27) of BA000023 from base 2100001 (BA000023 Sulfolobus tokodaii str. 7 DN

Query Match 83.6%; Score 18.4; DB 1; Length 110000;  
Best Local Similarity 95.0%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGCAACAGTGGCATGCACC 21  
||||||||||||| |||||  
Db 100593 TGGCAACAGTGGATGCACC 100612

RESULT 15

BA000023\_22

WPCOMMENT

Sequence split into 27 fragments LOCUS BA000023 Accession BA000023

Fragment Name	Begin	End
BA000023_00	1	110000
BA000023_01	100001	210000
BA000023_02	200001	310000
BA000023_03	300001	410000
BA000023_04	400001	510000
BA000023_05	500001	610000
BA000023_06	600001	710000
BA000023_07	700001	810000
BA000023_08	800001	910000
BA000023_09	900001	1010000
BA000023_10	1000001	1110000
BA000023_11	1100001	1210000
BA000023_12	1200001	1310000
BA000023_13	1300001	1410000
BA000023_14	1400001	1510000
BA000023_15	1500001	1610000
BA000023_16	1600001	1710000
BA000023_17	1700001	1810000
BA000023_18	1800001	1910000
BA000023_19	1900001	2010000
BA000023_20	2000001	2110000
BA000023_21	2100001	2210000
BA000023_22	2200001	2310000
BA000023_23	2300001	2410000
BA000023_24	2400001	2510000
BA000023_25	2500001	2610000
BA000023_26	2600001	2694756

Continuation (23 of 27) of BA000023 from base 2200001 (BA000023 Sulfolobus tokodaii str. 7 DN

Query Match 83.6%; Score 18.4; DB 1; Length 110000;  
Best Local Similarity 95.0%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGCAACAGTGGCATGCACC 21  
||||||||| |||||  
Db 593 TGGCAACAGTGGATGCACC 612

Search completed: May 7, 2006, 07:20:01  
Job time : 518.074 secs